Characterization of Pseudomonas syringae pv. actinidiae (Psa) isolated from France and assignment of Psa biovar 4 to a de novo pathovar:

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Résumé en anglais	Since 2008, bacterial canker of kiwifruit (Actinidia deliciosa and A. chinensis) caused by Pseudomonas syringae pv. actinidiae (Psa) has resulted in severe economic losses worldwide. Four biovars of Psa can be distinguished based on their biochemical, pathogenicity and molecular characteristics. Using a range of biochemical, molecular and pathogenicity assays, strains collected in France since the beginning of the outbreak in 2010 were found to be genotypically and phenotypically diverse, and to belong to biovar 3 or biovar 4. This is the first time that strains of biovar 4 have been isolated outside New Zealand or Australia. A multilocus sequence analysis based on four housekeeping genes (gapA, gltA, gyrB and rpoD) was performed on 72 strains representative of the French outbreak. All the strains fell into two phylogenetic groups: one clonal corresponding to biovar 3, and the other corresponding to biovar 4. This second phylogenetic group was polymorphic and could be divided into four lineages. A clonal genealogy performed with a coalescent approach did not reveal any common ancestor for the 72 Psa strains. Strains of biovar 4 are substantially different from those of the other biovars: they are less aggressive and cause only leaf spots whereas Psa biovars 1, 2 and 3 also cause canker and shoot die-back. Because of these pathogenic differences, which were supported by phenotypic, genetic and phylogenetic differences, it is proposed that Psa biovar 4 be renamed Pseudomonas syringae pv. actinidifoliorum pv. nov. Strain CFBP 8039 is designated as the pathotype strain
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